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TECH CENTER 1600/2900

#13

1645

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/591,447C

DATE: 04/08/2002
TIME: 16:09:02

Input Set : **A:\Sequence Listing 09591,447.txt**
Output Set: **N:\CRF3\04082002\I591447C.raw**

ENTERED

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 3 <110> APPLICANT: Chatfield, Steven N
 4        Dougan, Gordon
 5        Sydenham, Mark
 7 <120> TITLE OF INVENTION: Vaccines Containing Attenuated Bacteria
 9 <130> FILE REFERENCE: KCO1003US
11 <140> CURRENT APPLICATION NUMBER: US 09/591,447C
12 <141> CURRENT FILING DATE: 2000-06-09
14 <150> PRIOR APPLICATION NUMBER: UK 9726233.1
15 <151> PRIOR FILING DATE: 1997-12-11
17 <160> NUMBER OF SEQ ID NOS: 4
19 <170> SOFTWARE: MS-DOS
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22 <211> LENGTH: 1287
23 <212> TYPE: DNA
24 <213> ORGANISM: Salmonella typhimurium
26 <400> SEQUENCE: 1
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32 gacgttgatg gcttaatgca atcagtcaaa ctcaacgcgg gtcaggcagg tcagcagctt   180
34 ccggacgacg ccacgctgcg tcaccagatc ctggaacgtt tgattatgga tcaaattatc   240
36 ctgcagatgg gtcagaagat gggggtgaag atcacggatg agcagttgga tcagccatca   300
38 gccaacatcg ccaaacaaaa caatatgacg atggatcaga tgcgcagccg tctggcttac   360
40 gatgggctga actattcaac ctaccgtaac cagattcgta aagagatgat tatctctgaa   420
42 gtgcgcaaca atgaggttcg tcgccgtatc accgttttgc cgcaagaagt tgacgcgctg   480
44 gcaaaacaga ttggcacccca aaacgatgcc agcaccgagc tgaacctgag ccatatcctg   540
46 attgctctgc cggaaaaccc aacctccgag caggttaacg acgcgcagcg ccaggcggaa   600
48 agcattgttg aagaagcgcg taacggcgca gatttcggca aactggcgat tacctactct   660
50 gccgaccagc aggcgctaaa aggcggtcag atgggctggg gccgtatcca ggagctgccg   720
52 gggattttcg cccaggcgct gagcaccgcg aagaaaggcg acattgtcgg cccgattcgc   780
54 tccggcgtcg gcttccacat tctgaaagta aatgacctgc gcggtcagag ccagagtatc   840
56 tccgtgaccg aagttcacgc tcgtcacatt ctgcttaagc cgtcgccgat catgaacgat   900
58 cagcaggcgc gcctgaagct ggaagaaatc gcggctgaca ttaagagtgg taaaaccacc   960
60 tttgccgctg cggcgaaaga gtactctcag gacccgggct ccgctaacca gggcggtgat  1020
62 ttgggttggg ctacgccaga tattttcgac ccggcgttcc gcgacgcgct aacgaagctg  1080
64 cataaaggcc aaataagcgc gccggtacac tcctctttcg gctggcatct gatcgaattg  1140
66 ctggatacgc gtaaggtaga caaaaccgat gcggcgcaga aagatcgcgc ttatcgtatg  1200
68 ctgatgaacc gtaaattctc agaagaagcg gcgacctgga tgcaagaaca gcgcgccact  1260
70 tacgttaaga ttttgagtaa ctaatga                                       1287
73 <210> SEQ ID NO: 2
74 <211> LENGTH: 427
75 <212> TYPE: PRT
76 <213> ORGANISM: Salmonella typhimurium
78 <400> SEQUENCE: 2
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84              20                  25                  30
86  Asn Asn Gly Val Val Leu Glu Ser Asp Val Asp Gly Leu Met Gln Ser
87          35                  40                  45
89  Val Lys Leu Asn Ala Gly Gln Ala Gly Gln Gln Leu Pro Asp Asp Ala
90      50                  55                  60
92  Thr Leu Arg His Gln Ile Leu Glu Arg Leu Ile Met Asp Gln Ile Ile
93   65                  70                  75                  80
95  Leu Gln Met Gly Gln Lys Met Gly Val Lys Ile Thr Asp Glu Gln Leu
96              85                  90                  95
98  Asp Gln Pro Ser Ala Asn Ile Ala Lys Gln Asn Asn Met Thr Met Asp
99              100                 105                 110
101 Gln Met Arg Ser Arg Leu Ala Tyr Asp Gly Leu Asn Tyr Ser Thr Tyr
102             115                 120                 125
104 Arg Asn Gln Ile Arg Lys Glu Met Ile Ile Ser Glu Val Arg Asn Asn
105     130                 135                 140
107 Glu Val Arg Arg Arg Ile Thr Val Leu Pro Gln Glu Val Asp Ala Leu
108 145                 150                 155                 160
110 Ala Lys Gln Ile Gly Thr Gln Asn Asp Ala Ser Thr Glu Leu Asn Leu
111             165                 170                 175
113 Ser His Ile Leu Ile Ala Leu Pro Glu Asn Pro Thr Ser Glu Gln Val
114             180                 185                 190
116 Asn Asp Ala Gln Arg Gln Ala Glu Ser Ile Val Glu Glu Ala Arg Asn
117         195                 200                 205
119 Gly Ala Asp Phe Gly Lys Leu Ala Ile Thr Tyr Ser Ala Asp Gln Gln
120     210                 215                 220
122 Ala Leu Lys Gly Gly Gln Met Gly Trp Gly Arg Ile Gln Glu Leu Pro
123 225                 230                 235                 240
125 Gly Ile Phe Ala Gln Ala Leu Ser Thr Ala Lys Lys Gly Asp Ile Val
126             245                 250                 255
128 Gly Pro Ile Arg Ser Gly Val Gly Phe His Ile Leu Lys Val Asn Asp
129             260                 265                 270
131 Leu Arg Gly Gln Ser Gln Ser Ile Ser Val Thr Glu Val His Ala Arg
132         275                 280                 285
134 His Ile Leu Leu Lys Pro Ser Pro Ile Met Asn Asp Gln Gln Ala Arg
135     290                 295                 300
137 Leu Lys Leu Glu Glu Ile Ala Ala Asp Ile Lys Ser Gly Lys Thr Thr
138 305                 310                 315                 320
140 Phe Ala Ala Ala Ala Lys Glu Tyr Ser Gln Asp Pro Gly Ser Ala Asn
141             325                 330                 335
143 Gln Gly Gly Asp Leu Gly Trp Ala Thr Pro Asp Ile Phe Asp Pro Ala
144             340                 345                 350
146 Phe Arg Asp Ala Leu Thr Lys Leu His Lys Gly Gln Ile Ser Ala Pro
147         355                 360                 365
149 Val His Ser Ser Phe Gly Trp His Leu Ile Glu Leu Leu Asp Thr Arg
150     370                 375                 380
152 Lys Val Asp Lys Thr Asp Ala Ala Gln Lys Asp Arg Ala Tyr Arg Met
```

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153 385                    390                 395                      400
155 Leu Met Asn Arg Lys Phe Ser Glu Glu Ala Ala Thr Trp Met Gln Glu
156             405                 410 .              415
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159             420                 425
162 <210> SEQ ID NO: 3
163 <211> LENGTH: 1287
164 <212> TYPE: DNA
165 <213> ORGANISM: Escherichia coli
167 <400> SEQUENCE: 3
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173 gacgttgatg gattaatgca gtcggtaaaa ctgaacgctg ctcaggcaag gcagcaactt     180
175 cctgatgacg cgacgctgcg ccaccaaatc atggaacgtt tgatcatgga tcaaatcatt     240
177 ctgcagatgg ggcagaaaat gggagtgaaa atctccgatg agcagctgga tcaggcgatt     300
179 gctaacatcg cgaaacagaa caacatgacg ctggatcaga tgcgcagccg tctggcttac     360
181 gatggactga actacaacac ctatcgtaac cagatccgca aagagatgat tatctctgaa     420
183 gtgcgtaaca acgaggtgcg tcgtcgcatc accatcctgc cgcaggaagt cgaatccctg     480
185 gcgcagcagg tgggtaacca aaacgacgcc agcactgagc tgaacctgag ccacatcctg     540
187 atcccgctgc cggaaaaccc gacctctgat caggtgaacg aagcggaaag ccaggcgcgc     600
189 gccattgtcg atcaggcgcg taacggcgct gatttcggta agctggcgat tgctcattct     660
191 gccgaccagc aggcgctgaa cggcggccag atgggctggg gccgtattca ggagttgccc     720
193 gggatcttcg cccaggcatt aagcaccgcg aagaaaggcg acattgttgg cccgattcgt     780
195 tccggcgttg gcttccatat tctgaaagtt aacgacctgc gcggcgaaag caaaaatatc     840
197 tcggtgaccg aagttcatgc tcgccatatt ctgctgaaac cgtcgccgat catgactgac     900
199 gaacaggccc gtgtgaaact ggaacagatt gctgctgata tcgagagtgg taaaacgact     960
201 tttgctgccg caacgaaaga gttctctcag gatccagtct ctgctaacca gggcggcgat    1020
203 ctcggctggg ctacaccaga tattttcgat ccggccttcc gtgacgccct gactcgcctg    1080
205 aacaaaggtc aaatgagtgc accggttcac tcttcattcg gctggcattt aatcgaactg    1140
207 ctggataccc gtaatgtcga taaaaccgac gctgcgcaga aagatcgtgc ataccgcatg    1200
209 ctgatgaacc gtaagttctc ggaagaagca gcaagctgga tgcaggaaca acgtgccagc    1260
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215 <211> LENGTH: 428
216 <212> TYPE: PRT
217 <213> ORGANISM: Escherichia coli
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224 Thr Ser Phe Ala Ala Pro Gln Val Val Asp Lys Val Ala Ala Val Val
225             20                  25                  30
227 Asn Asn Gly Val Val Leu Glu Ser Asp Val Asp Gly Leu Met Gln Ser
228         35                  40                  45
230 Val Lys Leu Asn Ala Ala Gln Ala Arg Gln Gln Leu Pro Asp Asp Ala
231     50                  55                  60
233 Thr Leu Arg His Gln Ile Met Glu Arg Leu Ile Met Asp Gln Ile Ile
234 65                  70                  75                      80
236 Leu Gln Met Gly Gln Lys Met Gly Val Lys Ile Ser Asp Glu Gln Leu
237             85                  90                      95
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239 Asp Gln Ala Ile Ala Asn Ile Ala Lys Gln Asn Asn Met Thr Leu Asp
240             100             105             110
242 Gln Met Arg Ser Arg Leu Ala Tyr Asp Gly Leu Asn Tyr Asn Thr Tyr
243         115             120             125
245 Arg Asn Gln Ile Arg Lys Glu Met Ile Ile Ser Glu Val Arg Asn Asn
246     130             135             140
248 Glu Val Arg Arg Arg Ile Thr Ile Leu Pro Gln Glu Val Glu Ser Leu
249 145             150             155             160
251 Ala Gln Gln Val Gly Asn Gln Asn Asp Ala Ser Thr Glu Leu Asn Leu
252             165             .170             175
254 Ser His Ile Leu Ile Pro Leu Pro Glu Asn Pro Thr Ser Asp Gln Val
255             180             185             190
257 Asn Glu Ala Glu Ser Gln Ala Arg Ala Ile Val Asp Gln Ala Arg Asn
258         195             200             205
260 Gly Ala Asp Phe Gly Lys Leu Ala Ile Ala His Ser Ala Asp Gln Gln
261     210             215             220
263 Ala Leu Asn Gly Gly Gln Met Gly Trp Gly Arg Ile Gln Glu Leu Pro
264 225             230             235             240
266 Gly Ile Phe Ala Gln Ala Leu Ser Thr Ala Lys Lys Gly Asp Ile Val
267             245             250             255
269 Gly Pro Ile Arg Ser Gly Val Gly Phe His Ile Leu Lys Val Asn Asp
270             260             265             270
272 Leu Arg Gly Glu Ser Lys Asn Ile Ser Val Thr Glu Val His Ala Arg
273         275             280             285
275 His Ile Leu Leu Lys Pro Ser Pro Ile Met Thr Asp Glu Gln Ala Arg
276     290             295             300 ·
278 Val Lys Leu Glu Gln Ile Ala Ala Asp Ile Glu Ser Gly Lys Thr Thr
279 305             310             315             320
281 Phe Ala Ala Ala Thr Lys Glu Phe Ser Gln Asp Pro Val Ser Ala Asn
282             325             330             335
284 Gln Gly Gly Asp Leu Gly Trp Ala Thr Pro Asp Ile Phe Asp Pro Ala
285             340             345             350
287 Phe Arg Asp Ala Leu Thr Arg Leu Asn Lys Gly Gln Met Ser Ala Pro
288         355             360             365
290 Val His Ser Ser Phe Gly Trp His Leu Ile Glu Leu Leu Asp Thr Arg
291     370             375             380
293 Asn Val Asp Lys Thr Asp Ala Ala Gln Lys Asp Arg Ala Tyr Arg Met
294 385             390             395             400
296 Leu Met Asn Arg Lys Phe Ser Glu Glu Ala Ala Ser Trp Met Gln Glu
297             405             410             415
299 Gln Arg Ala Ser Ala Tyr Val Lys Ile Leu Ser Asn
300             420             425
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VERIFICATION SUMMARY   DATE: 04/08/2002
PATENT APPLICATION: US/09/591,447C   TIME: 16:09:03

Input Set : **A:\Sequence Listing 09591,447.txt**
Output Set: **N:\CRF3\04082002\I591447C.raw**

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date